OIPE

02-60

Input Set: I464039.RAW

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

P. 5

ENTERED

```
 1   <110> APPLICANT: Meyers, Rachel
 2   <120> TITLE OF INVENTION: 21612, 21615, 21620, 21676, 33756, Novel
 3         Human Alcohol Dehydrogenases
 4   <130> FILE REFERENCE: 5800-49
 5   <140> CURRENT APPLICATION NUMBER: US/09/464,039
 6   <141> CURRENT FILING DATE: 1999-12-15
 7   <160> NUMBER OF SEQ ID NOS: 10
 8   <170> SOFTWARE: FastSEQ for Windows Version 3.0
 9   <210> SEQ ID NO 1
10   <211> LENGTH: 260
11   <212> TYPE: PRT
12   <213> ORGANISM: Homo sapiens
13   <400> SEQUENCE: 1
14        Met Ala Arg Pro Gly Met Glu Arg Trp Arg Asp Arg Leu Ala Leu Val
15        1               5                   10                  15
16        Thr Gly Ala Ser Gly Gly Ile Gly Ala Ala Val Ala Arg Ala Leu Val
17                    20                  25                  30
18        Gln Gln Gly Leu Lys Val Val Gly Cys Ala Arg Thr Val Gly Asn Ile
19                    35                  40                  45
20        Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr Pro Gly Thr Leu
21                    50                  55                  60
22        Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu Asp Ile Leu Ser Met
23        65                  70                  75                  80
24        Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile Asn
25                    85                  90                  95
26        Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr Ser
27                    100                 105                 110
28        Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile Cys
29                    115                 120                 125
30        Thr Arg Glu Ala Tyr Gln Ser Met Lys Glu Arg Asn Val Asp Asp Gly
31                    130                 135                 140
32        His Ile Ile Asn Ile Asn Ser Met Ser Gly His Arg Val Leu Pro Leu
33        145                 150                 155                 160
34        Ser Val Thr His Phe Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala Leu
35                    165                 170                 175
36        Thr Glu Gly Leu Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile Arg
37                    180                 185                 190
38        Ala Thr Cys Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe Lys
39                    195                 200                 205
40        Leu His Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln Met
41                    210                 215                 220
42        Lys Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val Leu
43        225                 230                 235                 240
44        Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro Thr
```

```
45                          245            250              255
46          Glu Gln Val Thr
47                          260
48   <210> SEQ ID NO 2
49   <211> LENGTH: 1909
50   <212> TYPE: DNA
51   <213> ORGANISM: Homo sapiens
52   <220> FEATURE:
53   <221> NAME/KEY: misc_feature
54   <222> LOCATION: (0)...(0)
55   <223> OTHER INFORMATION: 21620 ADH
56   <220> FEATURE:
57   <221> NAME/KEY: CDS
58   <222> LOCATION: (421)...(1203)
59   <221> NAME/KEY: misc_feature
60   <222> LOCATION: (1)...(1909)
61   <223> OTHER INFORMATION: n = A,T,C or G
62   <400> SEQUENCE: 2
63          tacttagact cagccggctt ttccacgctt tgcctgaccc tgctttgctc aactgtacgt    60
64          cttgtttcgt tttctgttct gcgccgttac agatccaagc tctgaaaaac cagaaagtta   120
65          actggtaagt ttagtctttt tgtctttttat ttcaggtccc ggatccggtg atccaaatct   180
66          aagaactgct cctcagtgag tgttgccttt acttctaggc ctgtacggaa gtgttacttc   240
67          tgctctaaaa gctgcggaat tctaatacga ctcactatag ggagtcgacc cacgcgtccg   300
68          gggtctaggc gcggatcgga cccaagcagg tcggcggcgg cggcaggaga gcggccgggc   360
69          gtcagctcct cgacccccgt gtcgggctag tccagcgagg cggacgggcg cgtgggccc    420
70          atg gcc agg ccc ggc atg gag cgg tgg cgc gac cgg ctg gcg ctg gtg      468
71          Met Ala Arg Pro Gly Met Glu Arg Trp Arg Asp Arg Leu Ala Leu Val
72           1               5                  10                  15
73          acg ggg gcc tcg ggg ggc atc ggc gcg gcc gtg gcc cgg gcc ctg gtc      516
74          Thr Gly Ala Ser Gly Gly Ile Gly Ala Ala Val Ala Arg Ala Leu Val
75                          20                  25                  30
76          cag cag gga ctg aag gtg gtg ggc tgc gcc cgc act gtg ggc aac atc      564
77          Gln Gln Gly Leu Lys Val Val Gly Cys Ala Arg Thr Val Gly Asn Ile
78                       35                  40                  45
79          gag gag ctg gct gct gaa tgt aag agt gca ggc tac ccc ggg act ttg      612
80          Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr Pro Gly Thr Leu
81                       50                  55                  60
82          atc ccc tac aga tgt gac cta tca aat gaa gag gac atc ctc tcc atg      660
83          Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu Asp Ile Leu Ser Met
84           65                  70                  75                  80
85          ttc tca gct atc cgt tct cag cac agc ggt gta gac atc tgc atc aac      708
86          Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile Asn
87                       85                  90                  95
88          aat gct ggc ttg gcc cgg cct gac acc ctg ctc tca ggc agc acc agt      756
89          Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr Ser
90                      100                 105                 110
91          ggt tgg aag gac atg ttc aat gtg aac gtg ctg gcc ctc agc atc tgc      804
92          Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile Cys
93                      115                 120                 125
94          aca cgg gaa gcc tac cag tcc atg aag gag cgg aat gtg gac gat ggg      852
```

```
 95        Thr Arg Glu Ala Tyr Gln Ser Met Lys Glu Arg Asn Val Asp Asp Gly
 96            130                 135                 140
 97        cac atc att aac atc aat agc atg tct ggc cac cga gtg tta ccc ctg    900
 98        His Ile Ile Asn Ile Asn Ser Met Ser Gly His Arg Val Leu Pro Leu
 99        145                 150                 155                 160
100        tct gtg acc cac ttc tat agt gcc acc aag tat gcc gtc act gcg ctg    948
101        Ser Val Thr His Phe Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala Leu
102                        165                 170                 175
103        aca gag gga ctg agg caa gag ctt cgg gag gcc cag acc cac atc cga    996
104        Thr Glu Gly Leu Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile Arg
105                        180                 185                 190
106        gcc acg tgc atc tct cca ggt gtg gtg gag aca caa ttc gcc ttc aaa   1044
107        Ala Thr Cys Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe Lys
108                    195                 200                 205
109        ctc cac gac aag gac cct gag aag gca gct gcc acc tat gag caa atg   1092
110        Leu His Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln Met
111                210                 215                 220
112        aag tgt ctc aaa ccc gag gat gtg gcc gag gct gtt atc tac gtc ctc   1140
113        Lys Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val Leu
114        225                 230                 235                 240
115        agc act ccc gca cac atc cag att gga gac atc cag atg agg ccc acg   1188
116        Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro Thr
117                        245                 250                 255
118        gag cag gtg acc tag tgactgtggg agctcctcct tccctcccca cccttcatgg   1243
W-->119    Glu Gln Val Thr
120                        260
121        cttgcctcct gcctctggat tttaggtgtt gatttctgga tcacgggata ccacttcctg   1303
122        tccacacccc gaccaggggc tagaaaattt gtttgagatt tttatatcat cttgtcaaat   1363
123        tgcttcagtt gtaaatgtga aaaatgggct ggggaaagga ggtggtgtcc ctaattgttt   1423
124        tacttgttaa cttgttcttg tgcccctggg cacttggcct ttgtctgctc tcagtgtctt   1483
125        ccctttgaca tgggaaagga gttgtggcca aaatccccat cttcttgcac ctcaacgtct   1543
W-->126    gtggctyang ggctggggtg gcagagggag gccttcacct tatatctgtg ttgttatcca   1603
127        gggctccaga cttcctcctc tgcctgcccc actgcaccct ctccccctta tctatctcct   1663
128        tctcggctcc ccagcccagt cttggcttct tgtcccctcc tggggtcatc cctccactct   1723
129        gactctgact atggcagcag aacaccaggg cctggcccag tggatttcat ggtgatcatt   1783
130        aaaaaagaaa aatcgcaacc aaaaaaaaaa aaaaagggc gggccgctag actagtytag   1843
W-->131    agaaaaaacc tcccacacct ccccybdamm ytkacgccgn acgcnanggg ggcaatcaag   1903
132        gacgct                                                             1909
133  <210> SEQ ID NO 3
134  <211> LENGTH: 260
135  <212> TYPE: PRT
136  <213> ORGANISM: Homo sapiens
137  <400> SEQUENCE: 3
138        Met Glu Lys Cys Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu
139        1                 5                   10                  15
140        Asn His His Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser
141                        20                  25                  30
142        Ile Arg Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Arg Val Asp
143                35                  40                  45
144        Ile Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
```

```
145                 50                    55                    60
146           Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His Phe
147           65                    70                    75                    80
148           Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala Pro Ser
149                               85                    90                    95
150           Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly His Ile Asp
151                           100                   105                   110
152           Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn Thr Lys Ala Ala
153                       115                   120                   125
154           Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe Thr Lys Glu Leu Ser
155               130                   135                   140
156           Arg Arg Leu Gln Gly Ser Gly Val Thr Val Asn Ala Leu His Pro Gly
157           145                   150                   155                   160
158           Val Ala Arg Thr Glu Leu Gly Arg His Thr Gly Ile His Gly Ser Thr
159                           165                   170                   175
160           Phe Ser Ser Thr Thr Leu Gly Pro Ile Phe Trp Leu Leu Val Lys Ser
161                       180                   185                   190
162           Pro Glu Leu Ala Ala Gln Pro Ser Thr Tyr Leu Ala Val Ala Glu Glu
163                   195                   200                   205
164           Leu Ala Asp Val Ser Gly Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala
165               210                   215                   220
166           Pro Ala Pro Glu Ala Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala
167           225                   230                   235                   240
168           Glu Ser Ala Arg Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln
169                           245                   250                   255
170           Pro Leu Pro Arg
171                           260
172      <210> SEQ ID NO 4
173      <211> LENGTH: 1153
174      <212> TYPE: DNA
175      <213> ORGANISM: Homo sapiens
176      <220> FEATURE:
177      <221> NAME/KEY: misc_feature
178      <222> LOCATION: (0)...(0)
179      <223> OTHER INFORMATION: 33756 ADH
180      <220> FEATURE:
181      <221> NAME/KEY: CDS
182      <222> LOCATION: (265)...(1047)
183      <221> NAME/KEY: misc_feature
184      <222> LOCATION: (1)...(1153)
185      <223> OTHER INFORMATION: n = A,T,C or G
186      <400> SEQUENCE: 4
```

```
W-->  187      ccgcgccccg ccctcgcagc ccanntncgg acgcgggccc agccgcgcct gcgcttccgc      60
W-->  188      tcgcctgtgg ctgcaannag cgcgctcttc ctcggagcta cccaggcggc tggtgtagca     120
      189      gcaagctccg cgccgacccc tgacgcctga cgcctgtccc cggcccggca tgagccgcta     180
      190      cctgctgccg ctgtcggcgc tgggcacggt agcaggcgct cgccgtgctg ctcaagaggc     240
      191      aacatcatcc tggcctgccg agac atg gag aag tgt gag gcg gca gca aag     291
      192                                    Met Glu Lys Cys Glu Ala Ala Ala Lys
      193                                    1                   5
      194      gac atc cgc ggg gag acc ctc aat cac cat gtc aac gcc cgg cac ctg     339
```

```
195        Asp Ile Arg Gly Glu Thr Leu Asn His His Val Asn Ala Arg His Leu
196         10              15                  20                  25
197        gac ttg gct tcc ctc aag tct atc cga gag ttt gca gca aag atc att    387
198        Asp Leu Ala Ser Leu Lys Ser Ile Arg Glu Phe Ala Ala Lys Ile Ile
199                         30                  35                  40
200        gaa gag gag gag cga gtg gac att cta atc aac aac gcg ggt gtg atg    435
201        Glu Glu Glu Glu Arg Val Asp Ile Leu Ile Asn Asn Ala Gly Val Met
202                         45                  50                  55
203        cgg tgc ccc cac tgg acc acc gag gac ggc ttc gag atg cag ttt ggc    483
204        Arg Cys Pro His Trp Thr Thr Glu Asp Gly Phe Glu Met Gln Phe Gly
205                         60                  65                  70
206        gtt aac cac ctg ggt cac ttt ctc ttg aca aac ttg ctg ctg gac aag    531
207        Val Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys
208                 75                  80                  85
209        ctg aaa gcc tca gcc cct tcg cgg atc atc aac ctc tcg tcc ctg gcc    579
210        Leu Lys Ala Ser Ala Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala
211         90                  95                  100                 105
212        cat gtt gct ggg cac ata gac ttt gac gac ttg aac tgg cag acg agg    627
213        His Val Ala Gly His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg
214                         110                 115                 120
215        aag tat aac acc aaa gcc gcc tac tgc cag agc aag ctc gcc atc gtc    675
216        Lys Tyr Asn Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val
217                         125                 130                 135
218        ctc ttc acc aag gag ttg agc cgg cgg ctg caa ggc tct ggt gtg act    723
219        Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr
220                         140                 145                 150
221        gtc aac gcc ctg cac ccc ggc gtg gcc agg aca gag ctg ggc aga cac    771
222        Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
223                 155                 160                 165
224        acg ggc atc cat ggc tcc acc ttc tcc agc acc aca ctc ggg ccc atc    819
225        Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro Ile
226         170                 175                 180                 185
227        ttc tgg ctg ctg gtc aag agc ccc gag ctg gcc gcc cag ccc agc aca    867
228        Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro Ser Thr
229                         190                 195                 200
230        tac ctg gcc gtg gcg gag gaa ctg gcg gat gtt tcc gga aag tac ttc    915
231        Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly Lys Tyr Phe
232                         205                 210                 215
233        gat gga ctc aaa cag aag gcc ccg gcc ccc gag gct gag gat gag gag    963
234        Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala Glu Asp Glu Glu
235                         220                 225                 230
236        gtg gcc cgg agg ctt tgg gct gaa agt gcc cgc ctg gtg ggc tta gag   1011
237        Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg Leu Val Gly Leu Glu
238                 235                 240                 245
239        gct ccc tct gtg agg gag cag ccc ctc ccc aga taa cctctggagc        1057
W--> 240   Ala Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
241         250             255                 260
242        agatttgaaa gccaggatgg cgcctccaga ccgaggacag ctgtccgcca tgcccgcagc  1117
243        ttcctggcac tacctgagcc gggagaccca ggactg                           1153
```

<210> SEQ ID NO 5

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Line	?	Error/Warning	Original Text
119	W	Line data has been corrected	Glu Gln Val Thr *
126	W	"N" or "Xaa" used: Feature required	gtggctyang ggctggggtg gcagagggag gccttcac
131	W	"N" or "Xaa" used: Feature required	agaaaaaacc tcccacacct ccccybdamm ytkacgcc
187	W	"N" or "Xaa" used: Feature required	ccgcgccccg ccctcgcagc ccanntncgg acgcgggc
188	W	"N" or "Xaa" used: Feature required	tcgcctgtgg ctgcaannag cgcgctcttc ctcggagc
240	W	Line data has been corrected	Ala Pro Ser Val Arg Glu Gln Pro Leu Pro A
306	W	"N" or "Xaa" used: Feature required	gcntgtgggt cccttcttna aattgggtcc ccccgttt
307	W	"N" or "Xaa" used: Feature required	gttcaaagac nggncctttt gtcgggggct ccttgaag
308	W	"N" or "Xaa" used: Feature required	gctttttttt ttgggggncc cccccctttg ggaacccc
378	W	Line data has been corrected	Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
457	W	"N" or "Xaa" used: Feature required	aactccgccc atcccgcccc taactccgnc ccagttcc
547	W	Line data has been corrected	Lys Leu Glu Lys Leu Met Asn Gln Met Asn A
610	W	"N" or "Xaa" used: Feature required	atgcaaaagc cgagnccgcc tcggcctcta agctattc
666	W	Line data has been corrected	Tyr Val Thr Gly Asn Pro Val Ile Ile Asp G

Input Set: I464039.RAW

Line	Original Text	Corrected Data
119	Glu Gln Val Thr *	Glu Gln Val Thr
240	Ala Pro Ser Val Arg Glu Gln Pro Leu Pro A	Ala Pro Ser Val Arg Glu Gln Pro Leu Pro A
378	Pro Ser Val Arg Glu Gln Pro Leu Pro Arg	Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
547	Lys Leu Glu Lys Leu Met Asn Gln Met Asn A	Lys Leu Glu Lys Leu Met Asn Gln Met Asn A
666	Tyr Val Thr Gly Asn Pro Val Ile Ile Asp G	Tyr Val Thr Gly Asn Pro Val Ile Ile Asp G